

Appl. No. : 10/657,022  
Filed : September 5, 2003

### AMENDMENTS TO THE SPECIFICATION

**Please amend Paragraph [0057] as follows:**

Figures 1A-C ~~show~~ is-a sequence alignment of NY-ESO-1 (SEQ ID NO: 611) and several similar protein sequences; AADO5202-CAG-3 (SEQ ID NO: 612), CAA11044-LAGE-1a (SEQ ID NO: 613), CAA10194-LAGE1s (SEQ ID NO: 614), CAA11043-LAGE1b (SEQ ID NO: 615), CAA10196-LAGE1L (SEQ ID NO: 616), AAH02883 CT-2 (SEQ ID NO: 617) and the consensus sequence (SEQ ID NO: 618).

**Please amend Paragraph [0064] as follows:**

~~Figures~~ Figure 7A, B, and C show results of N-terminal pool sequencing of a T=60 min. time point aliquot of the PSMA<sub>163-192</sub> (SEQ ID NO: 619) proteasomal digest.

**Please amend Paragraph [0066] as follows:**

Figure 9 shows results of N-terminal pool sequencing of a T=60 min. time point aliquot of the PSMA<sub>281-310</sub> (SEQ ID NO: 620) proteasomal digest.

**Please amend Paragraph [0075] as follows:**

Figures 18-70 (SEQ ID NOS: 621-673, respectively) are proteasomal digestion maps depicting the mapping of mass spectrum peaks from the digest onto the sequence of the indicated substrate.

Please amend Table 4 as follows (please note that the new column with the heading "SEQ ID NO:" has been added to the table. The title of the table, despite being underlined, has not been amended):

Table 4. SSX-2<sub>31-68</sub> Mass Peak Identification.

MS PEAK (measured)	PEPTIDE	SEQ ID NO:	SEQUENCE	CALCULATED MASS (MH <sup>+</sup> )
988.23	31-37	<u>674</u>	YFSKEEW	989.08
1377.68±2.3 8	31-40	<u>675</u>	YFSKEEWEKM	1377.68
1662.45±1.3 0	31-43	<u>676</u>	YFSKEEWEKMKAS	1663.90
2181.72±0.8 5	31-47	<u>677</u>	YFSKEEWEKMKASEKIF	2181.52
2346.6	31-48	<u>678</u>	YFSKEEWEKMKASEKIFY	2344.71

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1472.16±1.5 4	38-49	<u>679</u>	EKKMKASEKIFYV	1473.77
2445.78±1.1 8	31-49*	<u>680</u>	YFSKEEWEKMKASEKIFYV	2443.84
2607.	31-50	<u>681</u>	YFSKEEWEKMKASEKIFYVY	2607.02
1563.3	50-61	<u>682</u>	YMKRKYEAMTKL	1562.93
3989.9	31-61	<u>683</u>	YFSKEEWEKMKASEKIFYVYMKRKYEAMTKL	3987.77
1603.74±1.5 3	51-63	<u>684</u>	MKRKYEAMTKLGF	1603.98
1766.45±1.5	50-63	<u>685</u>	YMKRKYEAMTKLGF	1767.16
1866.32±1.2 2	49-63	<u>686</u>	VYMKRKYEAMTKLGF	1866.29
4192.6	31-63	<u>687</u>	YFSKEEWEKMKASEKIFYVYMKRKYEAMTKLG F	4192.00
4392.1	31-65**	<u>688</u>	YFSKEEWEKMKASEKIFYVYMKRKYEAMTKLG FKA	4391.25

**Please amend Paragraph [0252] as follows:**

HLA-A\*0201 binding studies were performed with PSMA<sub>168-177</sub>, GMPEGDLVYV, (SEQ ID NO: 33) (SEQ ID NO: 33) essentially as described in Example 3 above. As seen in figure 8, this epitope exhibits significant binding at even lower concentrations than the positive control peptides. The Melan-A peptide used as a control in this assay (and throughout this disclosure), ELAGIGILTV (SEQ ID NO: 689), is actually a variant of the natural sequence (EAAGIGILTV (SEQ ID NO: 690)) and exhibits a high affinity in this assay.